STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _10/561,014_

Source: _1FWP_

Date Processed by STIC: _12/30/05_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 4.2.2 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
> http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
<u>Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:</u>

1. EFS-Bio (<u><http://www.uspto.gov/ebc/efs/downloads/documents.htm></u> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: _10/561,014_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____ Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 ____ Invalid Line Length

The rules require that a line **not exceed** 72 characters in length. This includes white spaces.

3 ____ Misaligned Amino
Numbering

The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.

4 ____ Non-ASCII

The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**

5 ____ Variable Length

Sequence(s) ____ contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____ PatentIn 2.0
"bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7 ____ Skipped Sequences
(OLD RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

8 ____ Skipped Sequences
(NEW RULES)

Sequence(s) _____ missing. If **intentional**, please insert the following lines for **each** skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 ____ Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.

10 ____ Invalid <213>
Response

Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence

11 ____ Use of <220>

Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12 ____ PatentIn 2.0
"bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ____ Misuse of n/Xaa

"n" can **only** represent a single <u>nucleotide</u>; "Xaa" can **only** represent a single <u>amino acid</u>

IFWP

RAW SEQUENCE LISTING   DATE: 12/30/2005
PATENT APPLICATION: US/10/561,014   TIME: 09:38:13

Input Set : A:\07039-409.txt
Output Set: N:\CRF4\12302005\J561014.raw

```
 4 <110> APPLICANT: Pan, Shuchong
 5        Simari, Robert D.
 7 <120> TITLE OF INVENTION: Isoforms of Brain Natriuretic Peptide
10 <130> FILE REFERENCE: 07039-409US1
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/561,014
C--> 12 <141> CURRENT FILING DATE: 2005-12-16
12 <150> PRIOR APPLICATION NUMBER: PCT/US2004/017554
13 <151> PRIOR FILING DATE: 2004-06-02
15 <150> PRIOR APPLICATION NUMBER: US 60/480,460
16 <151> PRIOR FILING DATE: 2003-06-20
18 <160> NUMBER OF SEQ ID NOS: 38
20 <170> SOFTWARE: FastSEQ for Windows Version 4.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 33
24 <212> TYPE: PRT
25 <213> ORGANISM: Homo sapiens
27 <400> SEQUENCE: 1
28 Gly Lys His Pro Leu Pro Pro Arg Pro Pro Ser Pro Ile Pro Val Cys
29 1               5                   10                  15
30 Asp Thr Val Arg Val Thr Leu Gly Phe Val Val Ser Gly Asn His Thr
31             20                  25                  30
32 Leu
35 <210> SEQ ID NO: 2
36 <211> LENGTH: 14
37 <212> TYPE: PRT
38 <213> ORGANISM: Homo sapiens
40 <400> SEQUENCE: 2
41 Val Val Gln Lys Glu Asn Gln Thr Phe Pro Pro Gly Phe Leu
42 1               5                   10
44 <210> SEQ ID NO: 3
45 <211> LENGTH: 162
46 <212> TYPE: PRT
47 <213> ORGANISM: Homo sapiens
49 <400> SEQUENCE: 3
50 Met Asp Pro Gln Thr Ala Pro Ser Arg Ala Leu Leu Leu Leu Leu Phe
51 1               5                   10                  15
52 Leu His Leu Ala Phe Leu Gly Gly Arg Ser His Pro Leu Gly Ser Pro
53             20                  25                  30
54 Gly Ser Ala Ser Asp Leu Glu Thr Ser Gly Leu Gln Glu Gln Arg Asn
55             35                  40                  45
56 His Leu Gln Gly Lys Leu Ser Glu Leu Gln Val Glu Gln Thr Ser Leu
57     50                  55                  60
58 Glu Pro Leu Gln Glu Ser Pro Arg Pro Thr Gly Val Trp Lys Ser Arg
```

```
59  65                    70                  75                    80
60  Glu Val Ala Thr Glu Gly Ile Arg Gly His Arg Lys Met Val Leu Tyr
61                     85                  90                    95
62  Thr Leu Arg Ala Pro Arg Ser Pro Lys Met Val Gln Gly Ser Gly Cys
63                    100                 105                   110
64  Phe Gly Arg Lys Met Asp Arg Ile Ser Ser Ser Ser Gly Leu Gly Cys
65             115                 120                   125
66  Lys Gly Lys His Pro Leu Pro Pro Arg Pro Pro Ser Pro Ile Pro Val
67        130                 135                 140
68  Cys Asp Thr Val Arg Val Thr Leu Gly Phe Val Val Ser Gly Asn His
69  145                 150                 155                   160
70  Thr Leu
73  <210> SEQ ID NO: 4
74  <211> LENGTH: 143
75  <212> TYPE: PRT
76  <213> ORGANISM: Homo sapiens
78  <400> SEQUENCE: 4
79  Met Asp Pro Gln Thr Ala Pro Ser Arg Ala Leu Leu Leu Leu Leu Phe
80   1                   5                  10                    15
81  Leu His Leu Ala Phe Leu Gly Gly Arg Ser His Pro Leu Gly Ser Pro
82                     20                  25                    30
83  Gly Ser Ala Ser Asp Leu Glu Thr Ser Gly Leu Gln Glu Gln Arg Asn
84             35                  40                    45
85  His Leu Gln Gly Lys Leu Ser Glu Leu Gln Val Glu Gln Thr Ser Leu
86        50                  55                  60
87  Glu Pro Leu Gln Glu Ser Pro Arg Pro Thr Gly Val Trp Lys Ser Arg
88  65                    70                  75                    80
89  Glu Val Ala Thr Glu Gly Ile Arg Gly His Arg Lys Met Val Leu Tyr
90                     85                  90                    95
91  Thr Leu Arg Ala Pro Arg Ser Pro Lys Met Val Gln Gly Ser Gly Cys
92                    100                 105                   110
93  Phe Gly Arg Lys Met Asp Arg Ile Ser Ser Ser Ser Gly Leu Gly Cys
94             115                 120                   125
95  Lys Val Val Gln Lys Glu Asn Gln Thr Phe Pro Pro Gly Phe Leu
96        130                 135                 140
98  <210> SEQ ID NO: 5
99  <211> LENGTH: 489
100 <212> TYPE: DNA
101 <213> ORGANISM: Homo sapiens
103 <400> SEQUENCE: 5
104 atggatcccc agacagcacc ttcccgggcg ctcctgctcc tgctcttctt gcatctggct    60
105 ttcctgggag gtcgttccca cccgctgggc agccccggtt cagcctcgga cttggaaacg   120
106 tccgggttac aggagcagcg caaccatttg cagggcaaac tgtcggagct gcaggtggag   180
107 cagacatccc tggagcccct ccaggagagc ccccgtccca caggtgtctg gaagtcccgg   240
108 gaggtagcca ccgagggcat ccgtgggcac cgcaaaatgg tcctctacac cctgcgggca   300
109 ccacgaagcc ccaagatggt gcaagggtct ggctgctttg ggaggaagat ggaccggatc   360
110 agctcctcca gtggcctggg ctgcaaaggt aagcacccccc tgccaccccg gccgccttcc   420
111 cccattccag tgtgtgacac tgttagagtc actttggggt ttgttgtctc tgggaaccac   480
112 actctttga                                                           489
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114 <210> SEQ ID NO: 6
115 <211> LENGTH: 432
116 <212> TYPE: DNA
117 <213> ORGANISM: Homo sapiens
119 <400> SEQUENCE: 6
120 atggatcccc agacagcacc ttcccgggcg ctcctgctcc tgctcttctt gcatctggct   60
121 ttcctgggag gtcgttccca cccgctgggc agccccggtt cagcctcgga cttggaaacg   120
122 tccgggttac aggagcagcg caaccatttg cagggcaaac tgtcggagct gcaggtggag   180
123 cagacatccc tggagcccct ccaggagagc ccccgtccca caggtgtctg gaagtcccgg   240
124 gaggtagcca ccgagggcat ccgtgggcac cgcaaaatgg tcctctacac cctgcgggca   300
125 ccacgaagcc ccaagatggt gcaagggtct ggctgctttg ggaggaagat ggaccggatc   360
126 agctcctcca gtggcctggg ctgcaaagtg gtgcagaaag agaaccaaac atttcctcct   420
127 ggtttcctct aa   432
129 <210> SEQ ID NO: 7
130 <211> LENGTH: 44
131 <212> TYPE: PRT
132 <213> ORGANISM: Pongo pygmaeus
134 <400> SEQUENCE: 7
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136 1   5   10   15
137 Asp Thr Val Arg Val Thr Leu Gly Phe Val Val Ser Gly Asn His Thr
138   20   25   30
139 Leu Arg Lys Cys His Leu Asp Ile Thr Ser Ser Cys
140   35   40
142 <210> SEQ ID NO: 8
143 <211> LENGTH: 58
144 <212> TYPE: PRT
145 <213> ORGANISM: Sus scrofa
147 <400> SEQUENCE: 8
148 Gly Glu His Pro Pro Pro Phe Pro Leu His Ala Pro Val Ser Ile Thr
149 1   5   10   15
150 Ser Gly Phe Asp Val Ser Gly Asp Gln Thr Pro Arg Lys Gly His Leu
151   20   25   30
152 Asp Ile Thr Leu Ser Cys Cys Gln Ser Ser Arg Pro Arg Ser Ala Phe
153   35   40   45
154 Leu Glu Lys Leu Asn Leu Asp Ser Ile His
155   50   55
157 <210> SEQ ID NO: 9
158 <211> LENGTH: 33
159 <212> TYPE: PRT
160 <213> ORGANISM: Pan troglodytes
162 <400> SEQUENCE: 9
163 Gly Glu His Pro Leu Pro Pro Arg Pro Pro Ser Pro Ile Pro Val Cys
164 1   5   10   15
165 Asp Thr Val Arg Val Thr Leu Gly Phe Val Val Ser Gly Asn His Thr
166   20   25   30
167 Leu
170 <210> SEQ ID NO: 10
171 <211> LENGTH: 78

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172 <212> TYPE: PRT
173 <213> ORGANISM: Ovis aries
175 <400> SEQUENCE: 10
176 Gly Glu Arg Leu Ser Ala Phe Pro Leu His Ile Thr Ile Arg Ala Thr
177 1               5                   10                  15
178 Ser Gly Ser Asp Val Ser Gly Asp Gln Ile Leu Asn Lys Glu His His
179             20                  25                  30
180 Ser Ser Leu Leu Ala Val Leu Arg Ala Lys Ala Cys Leu Ser Gly Asn
181         35                  40                  45
182 Ile Lys Phe Gly Gln His Ser Leu Ser Cys Leu Gly Ala Pro Ser Ile
183     .50                 55                  60
184 His Leu Leu Pro Leu Thr Glu Arg Gly Arg Ile Phe Arg Met
185 65                  70                  75
187 <210> SEQ ID NO: 11
188 <211> LENGTH: 26
189 <212> TYPE: PRT
190 <213> ORGANISM: Mus musculus
192 <400> SEQUENCE: 11
193 Gly Glu His Leu Pro Cys His Phe Pro Ala Lys Leu His Thr His Pro
194 1               5                   10                  15
195 Ile Pro Val His Ala Thr Leu Arg Gly Pro
196             20                  25
198 <210> SEQ ID NO: 12
199 <211> LENGTH: 33
200 <212> TYPE: PRT
201 <213> ORGANISM: Gorilla gorilla
203 <400> SEQUENCE: 12
204 Gly Glu His Pro Leu Pro Pro Arg Pro Pro Ser Pro Ile Pro Val Cys
205 1               5                   10                  15
206 Asp Thr Val Arg Val Thr Leu Gly Phe Val Val Ser Gly Asn His Thr
207             20                  25                  30
208 Leu
211 <210> SEQ ID NO: 13
212 <211> LENGTH: 86
213 <212> TYPE: PRT
214 <213> ORGANISM: Felis catus
216 <400> SEQUENCE: 13
217 Gly Lys Pro Pro Pro Cys Gln Leu Asp Pro Pro Ala Pro Leu Leu Trp
218 1               5                   10                  15
219 Val Pro Pro Ser Glu Pro Leu Leu Gly Leu Leu Ser Leu Gly Thr Asn
220             20                  25                  30
221 Ser Glu Lys Lys Thr Leu Gly Leu Tyr Ser Leu Leu Leu Thr Val Leu
222         35                  40                  45
223 Lys Ala Lys Gly Arg Leu Ser Gly Asn Ile Lys Cys Gly His His Ser
224     50                  55                  60
225 Leu Leu Cys Pro Pro Arg Val Thr His Leu Leu Leu Pro Leu Trp Pro
226 65                  70                  75                  80
227 Lys Gly Ala Glu Ser Pro
228             85
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230 <210> SEQ ID NO: 14
231 <211> LENGTH: 169
232 <212> TYPE: PRT
233 <213> ORGANISM: Canis familiaris
235 <400> SEQUENCE: 14
236 Met Glu Pro Cys Ala Ala Leu Pro Arg Ala Leu Leu Leu Leu Leu Phe
237 1               5                   10                  15
238 Leu His Leu Ser Pro Leu Gly Gly Arg Pro His Pro Leu Gly Gly Arg
239             20                  25                  30
240 Ser Pro Thr Ser Glu Ala Ser Glu Ala Ser Glu Ala Ser Gly Leu Trp
241         35                  40                  45
242 Ala Val Gln Glu Leu Leu Gly Arg Leu Lys Asp Ala Val Ser Glu Leu
243     50                  55                  60
244 Gln Ala Glu Gln Leu Ala Leu Glu Pro Leu His Arg Ser His Ser Pro
245 65                  70                  75                  80
246 Ala Glu Ala Pro Glu Ala Gly Glu Glu Arg Pro Val Gly Val Leu Ala
247             85                  90                  95
248 Pro His Asp Ser Val Leu Gln Ala Leu Arg Arg Leu Arg Ser Pro Lys
249             100                 105                 110
250 Met Met His Lys Ser Gly Cys Phe Gly Arg Arg Leu Asp Arg Ile Gly
251         115                 120                 125
252 Ser Leu Ser Gly Leu Gly Cys Asn Gly Lys Pro Pro Pro Cys His Leu
253     130                 135                 140
254 Gly Ser Pro Ser Pro Ala Pro Trp Val Arg Pro Leu Glu Pro Leu Leu
255 145                 150                 155                 160
256 Gly Leu Leu Ser Arg Gly Ile Thr Leu
257             165
259 <210> SEQ ID NO: 15
260 <211> LENGTH: 15
261 <212> TYPE: PRT
262 <213> ORGANISM: Dendoaspis angusticeps
264 <400> SEQUENCE: 15
265 Pro Ser Leu Arg Asp Pro Arg Pro Asn Ala Pro Ser Thr Ser Ala
266 1               5                   10                  15
268 <210> SEQ ID NO: 16
269 <211> LENGTH: 32
270 <212> TYPE: PRT
271 <213> ORGANISM: Homo sapiens
273 <400> SEQUENCE: 16
274 Ser Pro Lys Met Val Gln Gly Ser Gly Cys Phe Gly Arg Lys Met Asp
275 1               5                   10                  15
276 Arg Ile Ser Ser Ser Ser Gly Leu Gly Cys Lys Val Leu Arg Arg His
277             20                  25                  30
279 <210> SEQ ID NO: 17
280 <211> LENGTH: 41
281 <212> TYPE: PRT
282 <213> ORGANISM: Dendroaspis angusticeps
284 <400> SEQUENCE: 17
285 Glu Val Lys Tyr Asp Pro Cys Phe Gly His Lys Ile Asp Arg Ile Asn
```

```
<210> 20
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
<223> polypeptide
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insufficient explanation – give source of
genetic material

(see item 11 on

Error Summary
Sheet)

Input Set : **A:\07039-409.txt**
Output Set: **N:\CRF4\12302005\J561014.raw**

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:20; Xaa Pos. 2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23
Seq#:20; Xaa Pos. 24,25,26,27,28,29,31,32,33,34

Input Set : **A:\07039-409.txt**
Output Set: **N:\CRF4\12302005\J561014.raw**

L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:322 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:326 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:20
L:330 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:20
L:334 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:20
L:338 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:20
L:343 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:20
L:347 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:20
L:351 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:20
L:355 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:20
L:359 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:20
L:363 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:20
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L:371 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:20
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L:440 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:20
L:444 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:20
L:448 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:20
L:452 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:20
L:453 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20 after pos.:0
L:455 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20 after pos.:16
L:457 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20 after pos.:32